

Notch (C)	IDE \bar{C} -SNP	\bar{C} QNGGTC---D-V \bar{G} SY- \bar{C} - \bar{C} PP \bar{G} FT	GK--- \bar{C} E-N
<u>10244 (C)</u>	-NE \bar{C} TM---	\bar{C} QH--- \bar{C} VNT- \bar{G} SY- \bar{C} K \bar{C} -S \bar{G} --	\bar{G} --L- \bar{C} D
80		\bar{C} R \bar{C} FP \bar{G} YT	\bar{G} KT \bar{C} SQ D
95	VNE \bar{C} GKMPRP	\bar{C} QHR \bar{C} VNT \bar{H} \bar{G} SYK \bar{C} F \bar{C} LS	\bar{G} HMLMP D
133	VNSRTCAMIN	\bar{C} QYS \bar{C} EDT \bar{E} EPQ \bar{C} L \bar{C} PSS	\bar{G} LRLAPN
175	IDE \bar{C} ASGKVI	\bar{C} PYNRR \bar{C} VNT \bar{F} \bar{G} SY \bar{C} K \bar{C} HIGFE	LQYISGR
220	INE \bar{C} TMDSHT	\bar{C} SHHAN \bar{C} FNTQGSF \bar{C} K \bar{C} KQ \bar{G} YK	\bar{G} NGRL \bar{C} S
<u>CD97 (C)</u>	V-E \bar{C} -SG-Q-- \bar{C} -SS-- \bar{C}	-NTV \bar{G} SY- \bar{C} R \bar{C} RP \bar{G} W-P-P \bar{G} -PN---	D
<u>EGF (C)</u>	NSDSE \bar{C} PLSHDGY \bar{C} LHDGV \bar{C} MYIEALDKYA \bar{C} NCV \bar{G} YI---	\bar{G} ER-- \bar{C} QYRDLLKWWELR	

Figure 1

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
 SEQ ID NO: 1

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
 GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGACTCCGCC TGGCCCCAAA
 TGGAAGAGAC TGTCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT
 GTCCCTACAA TCGAAGATGT GTGAACACAT TTGGAAGCTA CTA CTGCAAAA
 TGTCACATTG GTTTCGAACT GCAATATATC AGTGGACGAT ATGACTGTAT
 AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA
 ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT
 AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA
 AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG
 CTCACAAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGTTACCCCA
 GAACCCACCA GGACTCCTAC CCCTAAGGTG AACTTGCAGC CCTTCAACTA
 TGAAGAGATA GTTTCAGAG GCGGGAACCTC TCATGGAGGT AAAAAAGGGA
 ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA
 GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT
 CCCTAAGGTG AATGAAGCAG GTGAATTCGG CCTGATTCTG GTCCAAAGGA
 AAGCGCTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTTGAC
 TGCAGCTTCA ATCATGGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA
 TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG
 CAGTTCCGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAAACTT
 CTCCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA
 CCGGCTGGCC GGAGACAAAG TCGGGAAACT TCGAGTGTTT GTGAAAAACA
 GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAAAGTGG
 AAGACAGGGA AAATTCAGTT GTATCAAGGA ACTGATGCTA CCAAAGCAT
 CATTTTTGAA GCAGAACGTG GCAAGGGCAA AACCGGCGAA ATCGCAGTGG
 ATGGCGTCTT GCTTGTTTCA GGCTTATGTC CAGATAGCCT TTTATCTGTG
 GANNNCTGAA TGGTACTATC TTTATATTTG ACTTTGTATG TCAGTTCCTT
 GGTTTTTTTTG ATATTGCATC ATAGGACCTC TGGCATTTTA AAATTACTAG
 CTGAAAAATT G
 SEQ ID NO: 2

FIGURE 2

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE
SEQ ID NO:3

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP
NGRDCLDIDECASGKVICPYNRRVCNTFGSYCKCHIGFELQYISGRYDCIDINECTMDS
HTCSHHANCFNTQGSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH
KNSMKKKAKIKNVTPEPTRTPKVNLPFNYEEIVSRGGNSHGGKKGNEEKMKEGLE
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISVDCSF
NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN
FCLLFDYRLAGDKVGKLRVFKNSNNALAWKTTSEDEKWKTGKIQLYQGTDATKSIIF
EAERGKGTGEIAVDGVLLVSGLCPSLLSVDDXMVLSLYLTLYVSSLVFLILHRTSGI
LKLLAEKL
SEQ ID NO:4

FIGURE 3

09981649.022802

20220" 54513660

ACTAGTGATTCCATCTAATACGACTCACATATAGGGCTCGAGCGCGCCCGGGCAGGTCTGCAGGACAGACCCCGGTA
ACTGCGAGTGGAGCGGAGACCCGAGCGGCTGAGGAGAGAGAGCGCGGCTTAGCTGCTACGGGGTCCGGCCGCGGCC
CTCCGAGGGGGCTCAGGAGGAGGAAGAGGACCCGCTGCGAGAAATGCCTCTGCCCTGGAGCCTTCGCGTCCCGCTGCTG
CTCCCTGGGTGGCAGGTGGTTTCGGGAACCGGGCCAGTCAAGGCATCAGGGTTGTTAGCATCGGCACGTCAAGCTGCG
GGTCTGTCACTATGGAACATAAATGGCTGCTGTACGGTGGAGAACACAGAGGAGTCTGTGAAGCTACATGCG
AACTGGATGTAACTTTGGTGAGTGGTGGACCAAAACAAATGCAGATGCTTTCAGGATACACCGGGAAAAACCTGCAGT
CAAGATGTGAATGAGTGTGAATGAATGAAACCCCGGCTATGCTACGCTGTGAACCTAGGACATGTGCCATGATAAATGTGACTACTA
TTGCCCTCAGTGGCCACATGCTCATGCCAGATGCTACGCTGTGAACCTCAGGACTCCGCTGCCCAATGGAAGAGACTGT
GCTGTGAAGACACAGAAGAGGGCCAGTGCCTGTGTCACTCATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTA
CTAGATAATTGATGAATGTGCCCTCTGTGTAAGTCACTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTA
CTGCAAAATGTCAATGGTTTCGAACCTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACTATGG
ATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAGGGTCTTCAAGTGAATGTAATGCAAGCAGGGATATAAA
GGCAATGGACTTTCGGTGTCTGCTATCCCTGAAAATTTCTGTGAAGGAAGTCTCAGAGCACCTGGTACCATCAAGACAG
AATCAAGAAATTGCTGTCTCAAAAACAGCATGAAAAGAGGCAAAAATTAATAATGTTACCCAGAACCCACCCAGGA
CTCTACCCCTAAGGTGAACCTTGACGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGGGGAACCTCATGGAGGTAAA
AAAGGGAATGAAGAGAAAATGAAGAGGGGCTTGAGGATGAGAAAAGAGAGAGAAAAGCCCTGAAGAAATGACWTAGAGGA
GCGAAGCCTCGAGGAGATGTGTTTTTCCCTAAGTGAATGAAGCAGGTGAATTCGGCTGATTTCTGGTCCAAAGGAAAG
CGCTAACTTCCAACTGGAAACATAAAGATTTAAATATCTCGTGTGACTGCGACTTCAATCATGGGATCTGTGACTGGA
CAGGATAGAGAAGATGTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGCTTCTATATGGCAGTTCGCGGCTT
GGCAGGTCACAAGAAACATTTGGCCGATTGAAAATTTCTCTACCTGACCTGCAACCCCAAGCAACTTCTGTTTGCTCT
TTGATTAACGGCTGGCCGAGACAAAGTCGGGAAAATTCAGTGTGTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAG
AAGACACGAGTAGGATGAAAAGTGGAAAGACAGGAAAAATTCAGTTGATCAAGGAACTGATGCTACCAAAAGCATCAT
TTTTGAAGCAGAAACCTGGCAAGGGCAAAACCGCGGAAATCGCAGTGGATGGCTCTTGCTTGTTCAGGCTTATGTCCAG
ATAGCCTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTTGACTTTGTATGTACGTTCCCTGGTGTTCCTGATA
TTGSATCATAGGACTCTGGCATTTTAAAAATTAAGCTGAAAAAATGTAAATGTACCAACAGAAATTTATTTGTAAGA
TGCCCTTMTTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCTTCTCAGTCATTTCTGAATCTTTC
CACATTATATTAATAATATGGAATGTGAGTTTATCTCCCTCCTCAGTATATCTGATTTGTATAAGTAAGTTGATGA
GCTTCTCTGCAACATTTCTAGAAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGTACTCTTATGATAGTTTT
TGGAAAACTATGACATCAAAGATAGACTTTTGGCTTAAGTGGCTTAGCTGGTCTTTCATAGCCAAACTTGTATATTTAAAT
TCTTTTGTATAATAATATCCAAATCATCAAAAAAATAAAAAA
SEQ ID NO: 5

MPLPWSLALPLLLPWAGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCEATCEPGCKFGEVGNKC
RCFPYGTGKTSQDNECGMKPRPCQHRCVNTGHSYKFCLSGHMLMPDATCVNSRSTCAMINQYSCEDTEEGPQCLCPS
SGLRLAPNGRDCLDIDECASGKVICPNRRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTWDSHTC SHHANCENTQ
GSFKCKQGYKGNGLRCSAIPENSVKELRAPGTIKDRIKLLAHKNSMKKAKIKNVTPEPTPTPKVNLQPFNYEE
IVSRGNSHGGKKGNEKMEGLEDEKREKALKNDXEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNLSV
DCSFNHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHKDIGRLKLLLPDLQPOSFCLLPDYRLAGDKVGLRV
FVKNSNALAWKTTTSEDEKWKTKGIQLYQGTDAKSIIFEAERGKGTGEIATVDGVLLVSLGCLPDSL SVDD

SEQ ID NO: 6

FIGURE 4

208220" 649T8660

**EGFL6 (221-260 aa)
3D Model**

**EGF
NMR Structure**

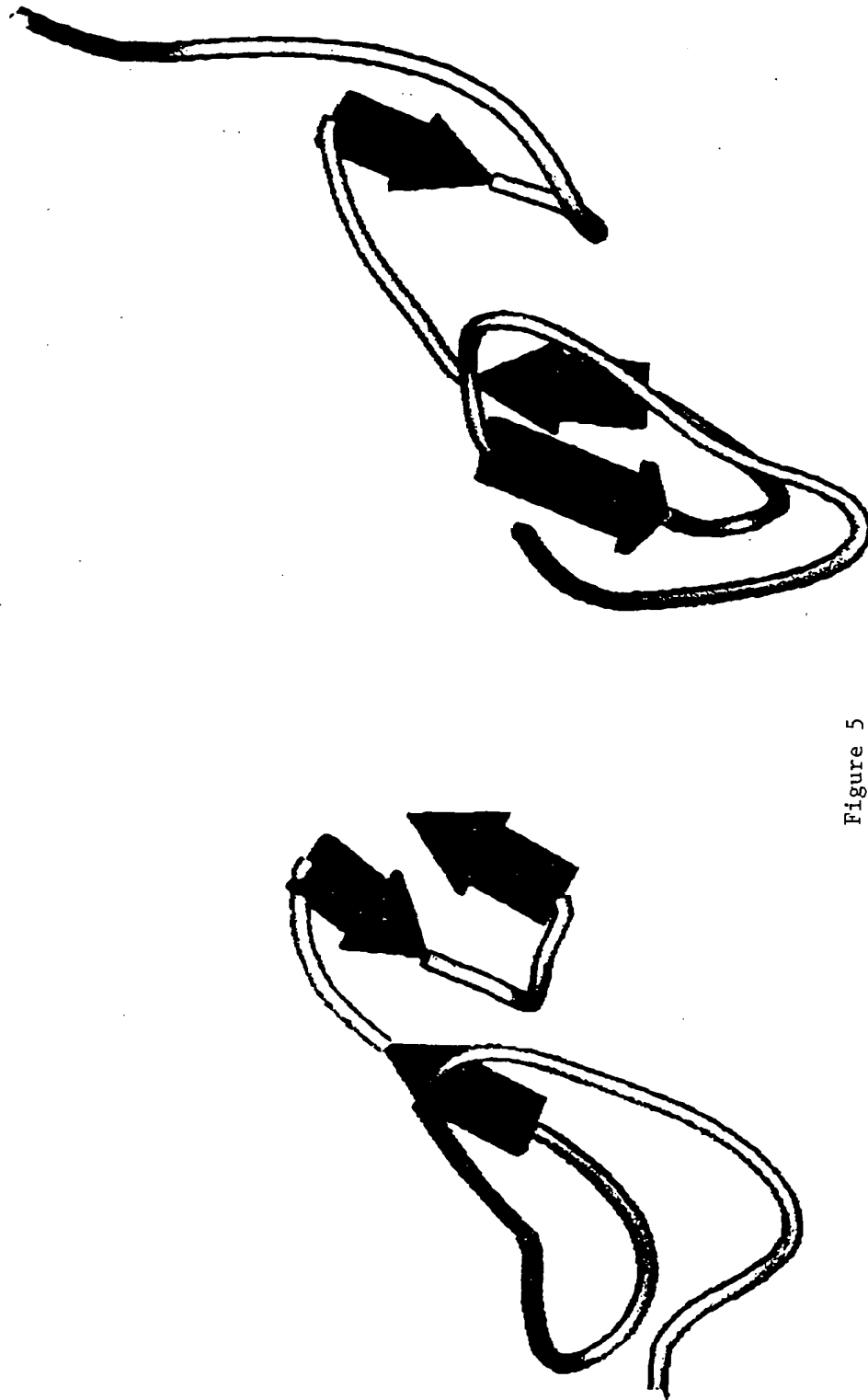


Figure 5